

#6



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/030,271

DATE: 08/21/2002

TIME: 15:44:48

Input Set : A:\217860US.ST25.txt

Output Set: N:\CRF4\08212002\J030271.raw

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3 <110> APPLICANT: OTA, TOSHIO
4   ISOGAI, TAKAO
5   NISHIKAWA, TETSUO
6   HIO, YURI
7   MIYOSHI, SOUSUKE
8   SATOH, SUSUMU
10 <120> TITLE OF INVENTION: APOPTOSIS-ASSOCIATED FACTOR
12 <130> FILE REFERENCE: 217860US0PCT
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/030,271
C--> 15 <141> CURRENT FILING DATE: 2002-06-28
17 <150> PRIOR APPLICATION NUMBER: JP 11-194179
18 <151> PRIOR FILING DATE: 1999-07-08
20 <150> PRIOR APPLICATION NUMBER: US 60/159,586
21 <151> PRIOR FILING DATE: 1999-10-18
23 <160> NUMBER OF SEQ ID NOS: 13
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 909
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
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33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(909)
35 <223> OTHER INFORMATION:
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43 tgc ctg gac tac tac ggg atg ctg tcg ctt cac cgt atg ttc gag gtg      96
44 Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu Val
45          20          25          30
47 gtg ggc ggg caa ctg acc gag tgc gag ctg gag ctc ctg gcc ttt ctg      144
48 Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Leu Ala Phe Leu
49          35          40          45
51 ctg gat gag gct cct ggc gcc gcc gga ggc tta gcc cgg gcc cgc agc      192
52 Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg Ser
53          50          55          60
55 ggc cta gag ctc ctg ctg gag ctg gag cgc cgc ggg cag tgc ggc gag      240
56 Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Gly Glu
57 65          70          75          80
59 agc aac ctg cgg ctg ctg ggg caa ctc ctg cgc gtg ctg gcc cgc cac      288
60 Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg His
61          85          90          95

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63 gac ctg ctg ccg cac ctg gcg cgc aag cgg cgc cgg cca gtg tct cca      336
64 Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser Pro
65      100      105      110
67 gaa cgc tat agc tat ggc acc tcc agc tct tca aag agg aca gag ggt      384
68 Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Ser Lys Arg Thr Glu Gly
69      115      120      125
71 agc tgc cgt cgc cgt cgg cag tca agc agt tct gca aat tct cag cag      432
72 Ser Cys Arg Arg Arg Arg Gln Ser Ser Ser Ser Ala Asn Ser Gln Gln
73      130      135      140
75 ggt cag tgg gag aca ggc tcc ccc cca acc aag cgg cag cgg cgg agt      480
76 Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg Ser
77 145      150      155      160
79 cgg ggc cgg ccc agt ggt ggt gcc aga cgg cgg cgg aga ggg gcc cca      528
80 Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Arg Gly Ala Pro
81      165      170      175
83 gcc gca ccc cag cag cag tca gag ccc gcc aga cct tcc tct gaa ggc      576
84 Ala Ala Pro Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu Gly
85      180      185      190
87 aaa gtg acc tgt gac atc cgg ctc cgg gtt cga gca gag tac tgc gag      624
88 Lys Val Thr Cys Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys Glu
89      195      200      205
91 cat ggg cca gcc ttg gag cag ggc gtg gca tcc cgg cgg ccc cag gcg      672
92 His Gly Pro Ala Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln Ala
93      210      215      220
95 ctg gcg cgg cag ctg gac gtg ttt ggg cag gcc acc gca gtg ctg cgc      720
96 Leu Ala Arg Gln Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu Arg
97 225      230      235      240
99 tca agg gac ctg ggc tct gtg gtt tgt gac atc aag ttc tca gag ctc      768
100 Ser Arg Asp Leu Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu Leu
101      245      250      255
103 tcc tat ctg gac gcc ttc tgg ggc gac tac ctg agt ggc gcc ctg ctg      816
104 Ser Tyr Leu Asp Ala Phe Trp Gly Asp Tyr Leu Ser Gly Ala Leu Leu
105      260      265      270
107 cag gcc ctg cgg ggc gtg ttc ctg act gag gcc ctg cga gag gct gtg      864
108 Gln Ala Leu Arg Gly Val Phe Leu Thr Glu Ala Leu Arg Glu Ala Val
109      275      280      285
111 ggc cgg gag gct gtt cgc ctg ctg gtc agt gtg gat gag gct gac      909
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113      290      295      300
116 <210> SEQ ID NO: 2
117 <211> LENGTH: 303
118 <212> TYPE: PRT
119 <213> ORGANISM: Homo sapiens
121 <400> SEQUENCE: 2
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124 1      5      10      15
127 Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu Val
128      20      25      30
131 Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Leu Ala Phe Leu

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132          35          40          45
135 Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg Ser
136          50          55          60
139 Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Gly Glu
140 65          70          75          80
143 Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg His
144          85          90          95
147 Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser Pro
148          100          105          110
151 Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Ser Lys Arg Thr Glu Gly
152          115          120          125
155 Ser Cys Arg Arg Arg Arg Gln Ser Ser Ser Ser Ala Asn Ser Gln Gln
156          130          135          140
159 Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg Ser
160 145          150          155          160
163 Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Gly Ala Pro
164          165          170          175
167 Ala Ala Pro Gln Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu Gly
168          180          185          190
171 Lys Val Thr Cys Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys Glu
172          195          200          205
175 His Gly Pro Ala Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln Ala
176          210          215          220
179 Leu Ala Arg Gln Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu Arg
180 225          230          235          240
183 Ser Arg Asp Leu Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu Leu
184          245          250          255
187 Ser Tyr Leu Asp Ala Phe Trp Gly Asp Tyr Leu Ser Gly Ala Leu Leu
188          260          265          270
191 Gln Ala Leu Arg Gly Val Phe Leu Thr Glu Ala Leu Arg Glu Ala Val
192          275          280          285
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200 <211> LENGTH: 1883
201 <212> TYPE: DNA
202 <213> ORGANISM: Homo sapiens
204 <220> FEATURE:
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206 <222> LOCATION: (124)..(1101)
207 <223> OTHER INFORMATION:
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213 aggagtcatac ggacgccaga atctggccgg gttctgagct tgttccgcct cctcccccg      120
215 gga atg gcg cta tcc ggg tcg acc ccg gcc ccg tgc tgg gag gag gat      168
216 Met Ala Leu Ser Gly Ser Thr Pro Ala Pro Cys Trp Glu Glu Asp
217 1          5          10          15
219 gag tgc ctg gac tac tac ggg atg ctg tcg ctt cac cgt atg ttc gag      216
220 Glu Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu

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221	20	25	30	
223	gtg gtg ggc ggg caa ctg acc gag tgc gag ctg gag ctc ctg gcc ttt			264
224	Val Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Leu Ala Phe			
225	35	40	45	
227	ctg ctg gat gag gct cct ggc gcc gcc gga ggc tta gcc cgg gcc cgc			312
228	Leu Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg			
229	50	55	60	
231	agc ggc cta gag ctc ctg ctg gag ctg gag cgc cgc ggg cag tgc ggc			360
232	Ser Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Gly			
233	65	70	75	
235	gag agc aac ctg cgg ctg ctg ggg caa ctc ctg cgc gtg ctg gcc cgc			408
236	Glu Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg			
237	80	85	90	95
239	cac gac ctg ctg ccg cac ctg gcg cgc aag cgg cgc cgg cca gtg tct			456
240	His Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser			
241	100	105	110	
243	cca gaa cgc tat agc tat ggc acc tcc agc tct tca aag agg aca gag			504
244	Pro Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Ser Lys Arg Thr Glu			
245	115	120	125	
247	ggg agc tgc cgt cgc cgt cgg cag tca agc agt tct gca aat tct cag			552
248	Gly Ser Cys Arg Arg Arg Arg Gln Ser Ser Ser Ser Ala Asn Ser Gln			
249	130	135	140	
251	cag ggt cag tgg gag aca ggc tcc ccc cca acc aag cgg cag cgg cgg			600
252	Gln Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg			
253	145	150	155	
255	agt cgg ggc cgg ccc agt ggt ggt gcc aga cgg cgg cgg aga ggg gcc			648
256	Ser Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Arg Gly Ala			
257	160	165	170	175
259	cca gcc gca ccc cag cag cag tca gag ccc gcc aga cct tcc tct gaa			696
260	Pro Ala Ala Pro Gln Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu			
261	180	185	190	
263	ggc aaa gtg acc tgt gac atc cgg ctc cgg gtt cga gca gag tac tgc			744
264	Gly Lys Val Thr Cys Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys			
265	195	200	205	
267	gag cat ggg cca gcc ttg gag cag ggc gtg gca tcc cgg cgg ccc cag			792
268	Glu His Gly Pro Ala Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln			
269	210	215	220	
271	gcg ctg gcg cgg cag ctg gac gtg ttt ggg cag gcc acc gca gtg ctg			840
272	Ala Leu Ala Arg Gln Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu			
273	225	230	235	
275	cgc tca agg gac ctg ggc tot gtg gtt tgt gac atc aag ttc tca gag			888
276	Arg Ser Arg Asp Leu Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu			
277	240	245	250	255
279	ctc tcc tat ctg gac gcc ttc tgg ggc gac tac ctg agt ggc gcc ctg			936
280	Leu Ser Tyr Leu Asp Ala Phe Trp Gly Asp Tyr Leu Ser Gly Ala Leu			
281	260	265	270	
283	ctg cag gcc ctg cgg ggc gtg ttc ctg act gag gcc ctg cga gag gct			984
284	Leu Gln Ala Leu Arg Gly Val Phe Leu Thr Glu Ala Leu Arg Glu Ala			
285	275	280	285	

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289          290          295          300
291 tat gag gct ggc cgg cgc cgc ctg ttg ctg atg gag gag gaa ggg ggg      1080
292 Tyr Glu Ala Gly Arg Arg Arg Leu Leu Leu Met Glu Glu Glu Gly Gly
293          305          310          315
295 cgg cgc ccg aca gag gcc tcc tgatccagga ctggcaggat tgatcccacc      1131
296 Arg Arg Pro Thr Glu Ala Ser
297 320          325
299 tccaagtctc cgggccacct tctcctggga ggacgaccat ctctaccctc tgacagcccc      1191
301 tcccacagga tgtgggctct gaggcctaaa ccatttccag ctgagtttcc tcccagact      1251
303 cctcctaccc ccaggtgtgc ccccttagcc tccggaggcg ggggctgggc ctgtatctca      1311
305 gaagggaggg gcacagctac aactcacca aaggcccccc tgacattgt atctctgato      1371
307 ttgggctgtc tgactgtca caggtgcaca cactcgtca tgcacacact gcccctgctg      1431
309 agatcttccc tgggcctctg ccctggcctg cttcccagca cacacttctt tggcctaagg      1491
311 gcttctctct caggacctct aatttgacca caaccaacct gggcttcagc cacatcagtg      1551
313 ggcactggag ctggggtgca catggggcct gctcaccttg cccacacatc tccagccagc      1611
315 cagggccctg cccagcttca atttacagac ctgactctcc tcaccttccc ccctgctgtc      1671
317 cagagctgaa catagacttg cacttggatg tcacctggag tgtcacatgg gagtgttatg      1731
319 gcagcatcat accaaggcct actgttgcaac atggggccaa aaccagtaaa cagccacctt      1791
321 cttggaaaagg gaatgcaaag gctttggggg tgatggaaaa gaccttttac aaatgatacc      1851
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326 <210> SEQ ID NO: 4
327 <211> LENGTH: 326
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334 1          5          10          15
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338          20          25          30
341 Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Ala Phe Leu
342          35          40          45
345 Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg Ser
346          50          55          60
349 Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Gly Glu
350 65          70          75          80
353 Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg His
354          85          90          95
357 Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser Pro
358          100          105          110
361 Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Ser Lys Arg Thr Glu Gly
362          115          120          125
365 Ser Cys Arg Arg Arg Arg Gln Ser Ser Ser Ser Ala Asn Ser Gln Gln
366          130          135          140
369 Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg Ser
370 145          150          155          160
373 Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Arg Gly Ala Pro
374          165          170          175

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VERIFICATION SUMMARY

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Input Set : A:\217860US.ST25.txt

Output Set: N:\CRF4\08212002\J030271.raw

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date